

EXHIBIT 6

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DeCypher Results for Job: Smith-Waterman Similarity Search

Results by Query

Click on a query below to view its search results.

1394_PTH9903

Search Details

Results for: 1394_PTH9903; (Length=669/QuerySize=669)

[Return to query summary](#)

Maximum possible score for this scoring matrix and query: 6690.00

RANK	SCORES	QF	TARGET	LOCUS	NAME	ACCESSION#	TF	TARGET
P_SCORE	DESCRIPTION							
<u>1</u>	3455.00	C	gi 1787371 gb AE000213.1 AE00021	AE000213.1	D			
ecoli_ae	-1.0e+00		Escherichia coli K12 MG1655 section 103 of 400 of th					
<u>2</u>	246.00	D	gi 1787371 gb AE000213.1 AE00021	AE000213.1	D			
ecoli_ae	-1.0e+00		Escherichia coli K12 MG1655 section 103 of 400 of th					

RANK 1 Score = 3455.00 P_Score = -1.0e+00

Q = CGI_3078ws206512.seq QF = C #Q Symbols = 669

T = gi|1787371|gb|AE000213.1|AE00021 TF = D #T Symbols = 10959

A = AE000213.1

D = Escherichia coli K12 MG1655 section 103 of 400 of the complete genome

Identical Match = 500 Similar = 500 Total # Of Gaps = 4

Identity: Alignment = 75% Query = 74% Target = 4%

Similarity: Alignment = 75% Query = 74% Target = 4%

QS = 662 QE = 1 TS = 8606 TE = 9268

Q 662 TCCTT-AGGGGTAACATCCCGCCATTCCCCGTTTGCCAGCGAGTCCAGCGTATAGCTGCC
TCCTT A GT AC TC CGCCATTC CC TT GC AG TCCA G TA CC

T 8606 TCCTTAATCTGTCACTTCTCGCCATTCAACATTGGCAAGATTATCCAAAGAGTAATCACC

Q 603 CATGGCGTAGCGAATGAGTCGCAGGGTAGGGAAGCCACATGCGCAGTCATGCGCCTGAC

CAT GC TAGCGAAT AGTCGCAG GT GGGAAGCC ACATG GC GTCATGCG C AC
 T 8666 CATCGCATAGCGAATCAGTCGCAGCGTGGGGAAGCCAACATGGGCGGTTCATGCGGCGCAC
 Q 543 CTGTCCGGTTGCGGCCTTCATAAAGGGTGATTTTAAGCCAGCTGGTAGGAATGGATTTACG
 CTG CG TT CG CCTTCATA A GGTGAT TT AGCCAGCTGGT GGAAT TTT CG
 T 8726 CTGGCGATTACGTCCTTCATATAAGGTGATCTTCAGCCAGCTGGTGGGAATACTTTTGCG
 Q 483 CTCACGAATCGGCGGGTTGCGCGGCCACAGCCACTCGGGTTCATTACACGTTCAATACC
 TCACGAAT GG GG TT CGCGGCCA A CCAC CGGGTTC T AC G TC CC
 T 8786 TTCACGAATTGGTGGATTCCGCGGCCATAACCACGCGGGTTCGTCAACCAGCTCCGCGCC
 Q 423 AGCCGGCAGGGTGGGACCGTCGTTTCAGCGTTACGCCGTTGCGCA--GCTTTGCCAGCGAC
 GC GGCAGGGT GG CC TC TT A GTTACGCC TTGCGCA GCTT GCG C
 T 8846 GGCGGGCAGGGTAGGGCCATCATTTAAGGTTACGCCATTGCGCAAGGCTTCAAGTGCCTC
 Q 365 GCGTCGTCCGGCTCGCCTTCAACCTGCACATAGTAAATTTTTCCGGTACGTTTGCCCGGC
 GT GT GG CCTTC ACCTGCACATA TA ATTTTTCCGGT CGTTT CCCGGC
 T 8906 TTGT-GT-GGGAATACCTTCCACCTGCACATAATAGATTTTTCCGGTGCCTTTACCCGGC
 Q 305 TGAGTAAGCCTGGCCTGGAGCACGCCGTCATTGGTAAGGACCAGCAGCCCCTCGCTGTCTG
 TG GT A C GCCTG A C CGCCGT ATTGGT AG ACCAGCA CCC TCGCT TCG
 T 8964 TGGGTTAAACGCGCCTGCAACGCGCGCTTATTGGTCAGCACCAGCAACCCTTCGCTATCG
 Q 245 CGATCCAGACGTCCCGCTGCGTAGACTCCCTGTACGGGGATAAAGTCCTTCAGCGTGCTG
 CG TC AG CG CC GCTGC TA AC CCCTG AC GGGAT AA TC TT A GT TG
 T 9024 CCGTCAAGGCGACCTGCTGCATAAACACCCTGAACCGGGATGAATTCTTTTAATGTTTTG
 Q 185 CGCCCCGGCCTCGTCGGTAAACTGCGGCAATACATCGTAGGGTTTATTGAACAGTATGACC
 CG CCGGC TC TCGGT AACTGCGG A ACATCGTAGGGTTTATTGAACAG AT AC
 T 9084 CGTCCGGCTTCATCGGTGAAGTGCAGGAAGAACATCGTAGGGTTTATTGAACAGGATCACA
 Q 125 CGCGTTGGCTGGGGTTCTGGCGTTCTTCTGGTGGCTTGTCGTGAGCTGAATCGCTCAACC
 CGCGT GGCTGG TTC GG T C CTGGT G GT G GAGCTGAATCGCT AACC
 T 9144 CGCGTGGGCTGGTTTTCAGGTTTACGCCTGGTAGAACGTTGCGAGCTGAATCGCTTAACC
 Q 65 CCGTGTTTTCTAAAAGAAGTTTTCTGTCATGGTATTTTCAGGCGTTATCAATTGCCGCATT
 GGTG TTTCTAAAAGAAGTTTT CATGGTATTTTCAG TTAT AATTGCCGCATT
 T 9204 TGGTGATTTCTAAAAGAAGTTTTTTCATGGTATTTTCAGAGATTATGAATTGCCGCATT
 Q 5 ATAGC
 ATAGC
 T 9264 ATAGC

RANK 2 Score = 246.00 P_Score = -1.0e+00

Q = CGI_3078ws206512.seq QF = D #Q Symbols = 669

T = gi|1787371|gb|AE000213.1|AE00021 TF = D #T Symbols = 10959

A = AE000213.1

D = Escherichia coli K12 MG1655 section 103 of 400 of the complete genome

Identical Match = 197 Similar = 197 Total # Of Gaps = 22

Identity: Alignment = 52% Query = 29% Target = 1%

Similarity: Alignment = 52% Query = 29% Target = 1%

QS = 234 QE = 570 TS = 10054 TE = 10387

Q 234 ACGTCTGGATCGCGACAGCGAGGGGCTGCTGGTCCTTACCAATGACGGCGTGCTCCAGGC
 ACGTCTGG TCG G CAGCGA G T C G TT C AA GA CGTG C G
 T 10054 ACGTCTGGTTCGTG-CAGCGATCGAATAC--GCAATTGCTAACGA--TCGTGACTCTG--

 Q 294 CAGGCTTACTCAGCCGGGCAAACGTACCGGAA--AAATTTAC--TATGTGCAGGTTGAAG
 T ACTC G G CAAA G A C A AA TT AC A G GC G TT AAG
 T 10107 -----TGACTCTGGTGCACAAAGGCAACATCATGAAGTTCACCGAAGGAGC-GTTTAAAG

 Q 350 GCGAGCCGGACGACGCGTCGCTGGCAAAGCTGCGCAACGGCGTAACGCTGAACGACGGTC
 C G AC A G CGC G A AG T G CGG G A CTGA CGACGGT
 T 10161 ACTGGGGCTACCAGCTGGCGCGTGAAGAGTTTGG---CGGTGAA---CTGATCGACGGTG

 Q 410 CCACCCTGCCGGCTGGTATTGAACGTGTGAATGAACCCGAGTGGCTGTGGCCGCGCAACC
 C CC TG C TGAA GT T AA AACCCGA C TGGC G A C
 T 10215 GC-CCGTGGC-----TGAAAGT-TAAA--AACCCGA---ACACTGGCAAAGAGATC

 Q 470 CGCCGATT-----CGTGAGCGTAAATCCATTCCT--ACCAG-----CTGGCTT
 C ATT CGTGA G AT CATTCCT A CAG C GGCT
 T 10259 GTC--ATTAAAGACGTGATTGCTGATGCATTCCTGCAACAGATCCTGCTGCGTCCGGCTG

 Q 511 AAAATCA-----CCCTTTATGAAGCCGCAAC-----CGACAGGTCAGGCG-CATGAC
 AA AT A CCT TATGAA CC AAC C ACA TC G CG C TG C
 T 10317 AATATGATGTTATCGCCTGTATGAA--CCTGAACGGTGACTACATTTCTGACGCCCTGGC

 Q 558 TGCGCATGTGGGC
 GCGCA GT GGC
 T 10375 AGCGCAGGTTGGC

Job Details

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 [EXTEND PENALTY] -5
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[ALIGNMENT THRESHOLD] 20
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12:00:00 GMT; path=/; domain=tblast-m.genomecorp.com;

[JOB MESSAGES]

[END JOB STATUS]

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For assistance contact
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